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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/879,827A*

1643

DATE: 01/27/1999
TIME: 15:55:05

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> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

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 1                              SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5        (i) APPLICANT: Jofuku, K. Diane
 6                       Okamuro, Jack K.
 7
 8       (ii) TITLE OF INVENTION: Methods for Improving Seeds
 9
10      (iii) NUMBER OF SEQUENCES: 111
11
12       (iv) CORRESPONDENCE ADDRESS:
13            (A) ADDRESSEE: Townsend and Townsend and Crew LLP
14            (B) STREET: Two Embarcadero Center, Eighth Floor
15            (C) CITY: San Francisco
16            (D) STATE: California
17            (E) COUNTRY: USA
18            (F) ZIP: 94111-3834
19
20        (v) COMPUTER READABLE FORM:
21            (A) MEDIUM TYPE: Floppy disk
22            (B) COMPUTER: IBM PC compatible
23            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26       (vi) CURRENT APPLICATION DATA:
27            (A) APPLICATION NUMBER: US 08/879,827
28            (B) FILING DATE: 20-JUN-1997
29            (C) CLASSIFICATION:
30
31      (vii) PRIOR APPLICATION DATA:
32            (A) APPLICATION NUMBER: US 08/700,152
33            (B) FILING DATE: 20-AUG-1996
34
35     (viii) ATTORNEY/AGENT INFORMATION:
36            (A) NAME: Bastian, Kevin L.
37            (B) REGISTRATION NUMBER: 34,774
38            (C) REFERENCE/DOCKET NUMBER: 023070-067210US
39
40       (ix) TELECOMMUNICATION INFORMATION:
41            (A) TELEPHONE: (415) 576-0200
42            (B) TELEFAX: (415) 576-0300
43
44
45   (2) INFORMATION FOR SEQ ID NO:1:
46
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47          (i) SEQUENCE CHARACTERISTICS:
48              (A) LENGTH: 3 amino acids
49              (B) TYPE: amino acid
50              (C) STRANDEDNESS:
51              (D) TOPOLOGY: linear
52
53         (ii) MOLECULE TYPE: peptide
54
55
56         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
57
58         Tyr Arg Gly
59         1
60
61
62  (2) INFORMATION FOR SEQ ID NO:2:
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64          (i) SEQUENCE CHARACTERISTICS:
65              (A) LENGTH: 4 amino acids
66              (B) TYPE: amino acid
67              (C) STRANDEDNESS:
68              (D) TOPOLOGY: linear
69
70         (ii) MOLECULE TYPE: peptide
71
72
73         (ix) FEATURE:
74              (A) NAME/KEY: Modified-site
75              (B) LOCATION: 3
76              (D) OTHER INFORMATION: /product= "OTHER"
77                                    /note= "Xaa = Ala or Ser"
78
79         (ix) FEATURE:
80              (A) NAME/KEY: Modified-site
81              (B) LOCATION: 4
82              (D) OTHER INFORMATION: /product= "OTHER"
83                                    /note= "Xaa = Arg or His"
84
85
86         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
87
88         Trp Glu Xaa Xaa
89         1
90
91
92  (2) INFORMATION FOR SEQ ID NO:3:
93
94          (i) SEQUENCE CHARACTERISTICS:
95              (A) LENGTH: 1680 base pairs
96              (B) TYPE: nucleic acid
97              (C) STRANDEDNESS: single
98              (D) TOPOLOGY: linear
99
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100        (ii) MOLECULE TYPE: cDNA
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102
103        (ix) FEATURE:
104             (A) NAME/KEY: -
105             (B) LOCATION: 1..1680
106             (D) OTHER INFORMATION: /note= "Arabidopsis APETALA2 (AP2)"
107
108
109        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
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111    CTCTCTCTCT CTCTTTAGCT CTTTTTTTTT TTTTGTTTTC ATTAAAGTTT TTATTTTATT          60
112
113    TTCTACCAAC CAAAAGCTTT TCTCTTTGGT TTCTCTTATT TAGCTTCTAA CCTTGAGGAG         120
114
115    AATATACCAG AGGATTGAAG TTTGAACCTT CAAAGATCAA AATCAAGAAA CCAAAAAAAA         180
116
117    ACAAAAAAAA TGTGGGATCT AAACGACGCA CCACACCAAA CACAAAGAGA AGAAGAATCT         240
118
119    GAAGAGTTTT GTTATTCTTC ACCAAGTAAA CGGGTTGGAT CTTTCTCTAA TTCAAGCTCT         300
120
121    TCAGCTGTTG TTATCGAAGA TGGATCCGAT GACGATGAAC TTAACCGGGT CAGACCCAAT         360
122
123    AACCCACTTG TCACCCATCA GTTCTTCCCT GAGATGGATT CTAACGGCGG TGGTGTTGCT         420
124
125    TCTGGCTTTC CTCGGGCTCA CTGGTTTGGT GTTAAGTTTT GTCAGTCGGA TCTAGCCACC         480
126
127    GGATCGTCCG CGGGTAAAGC TACCAACGTT GCCGCTGCCG TAGTGGAGCC GGCACAGCCG         540
128
129    TTGAAAAAGA GTCGGCGTGG ACCAAGATCA AGAAGTTCTC AGTATAGAGG TGTTACGTTT         600
130
131    TACCGGCGTA CCGGAAGATG GGAATCTCAT ATTTGGGACT GTGGGAAACA AGTTTACTTA         660
132
133    GGTGGATTTG ACACTGCTCA TGCAGCAGCT CGAGCATATG ATAGAGCTGC TATTAAATTC         720
134
135    CGTGGAGTAG AAGCGGATAT CAATTTCAAC ATCGACGATT ATGATGATGA CTTGAAACAG         780
136
137    ATGACTAATT TAACCAAGGA AGAGTTCGTA CACGTACTTC GCCGACAAAG CACAGGCTTC         840
138
139    CCTCGAGGAA GTTCGAAGTA TAGAGGTGTC ACTTTGCATA AGTGTGGTCG TTGGGAAGCT         900
140
141    CGTATGGGTC AATTCTTAGG CAAAAAGTAT GTTTATTTGG GTTTGTTCGA CACCGAGGTC         960
142
143    GAAGCTGCTA GAGCTTACGA TAAAGCTGCA ATCAAATGTA ACGGCAAAGA CGCCGTGACC        1020
144
145    AACTTTGATC CGAGTATTTA CGATGAGGAA CTCAATGCCG AGTCATCAGG GAATCCTACT        1080
146
147    ACTCCACAAG ATCACAACCT CGATCTGAGC TTGGGAAATT CGGCTAATTC GAAGCATAAA        1140
148
149    AGTCAAGATA TGCGGCTCAG GATGAACCAA CAACAACAAG ATTCTCTCCA CTCTAATGAA        1200
150
151    GTTCTTGGAT TAGGTCAAAC CGGAATGCTT AACCATACTC CCAATTCAAA CCACCAATTT        1260
152
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153   CCGGGCAGCA GCAACATTGG TAGCGGAGGC GGATTCTCAC TGTTTCCGGC GGCTGAGAAC   1320
154
155   CACCGGTTTG ATGGTCGGGC CTCGACGAAC CAAGTGTTGA CAAATGCTGC AGCATCATCA   1380
156
157   GGATTCTCTC CTCATCATCA CAATCAGATT TTTAATTCTA CTTCTACTCC TCATCAAAAT   1440
158
159   TGGCTGCAGA CAAATGGCTT CCAACCTCCT CTCATGAGAC CTTCTTGAAT CTTTTATATT   1500
160
161   TTTAAGGTTT ATTATTATAT AAGAAAAACA AAAATGAACC TTTGAAATCC CCACATGTTC   1560
162
163   TTGGTCATTT CATTAATCAT CGGCTTATAT TTTGCTTATT TTCCCCTAAA TCCTCTTGTT   1620
164
165   AACTTAGGCG AACAAAAAAA ATTAATGGAA ATCTTTTTCC CTCCATCGGT TACAAAAATA   1680
166
167
168   (2) INFORMATION FOR SEQ ID NO:4:
169
170        (i) SEQUENCE CHARACTERISTICS:
171             (A) LENGTH: 67 amino acids
172             (B) TYPE: amino acid
173             (C) STRANDEDNESS:
174             (D) TOPOLOGY: linear
175
176       (ii) MOLECULE TYPE: peptide
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178
179       (ix) FEATURE:
180             (A) NAME/KEY: Peptide
181             (B) LOCATION: 1..67
182             (D) OTHER INFORMATION: /note= "AP2-R1 direct repeat at
183                                   positions 129 to 195"
184
185       (ix) FEATURE:
186             (A) NAME/KEY: Region
187             (B) LOCATION: 32..49
188             (D) OTHER INFORMATION: /note= "putative AP2-R1 amphipathic
189                                   alpha-helix (SEQ ID NO:6)"
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191
192       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
193
194        Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr Arg Arg Thr Gly Arg Trp
195        1               5                   10                  15
196
197        Glu Ser His Ile Trp Asp Cys Gly Lys Gln Val Tyr Leu Gly Gly Phe
198                    20                  25                  30
199
200        Thr Asp Ala His Ala Ala Ala Arg Ala Tyr Asp Arg Ala Ala Ile Lys
201                    35                  40                  45
202
203        Phe Arg Gly Val Glu Ala Asp Ile Asn Phe Asn Ile Asp Asp Tyr Asp
204            50                  55                  60
205
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206        Asp Asp Leu
207        65
208
209
210   (2) INFORMATION FOR SEQ ID NO:5:
211
212        (i) SEQUENCE CHARACTERISTICS:
213             (A) LENGTH: 68 amino acids
214             (B) TYPE: amino acid
215             (C) STRANDEDNESS:
216             (D) TOPOLOGY: linear
217
218       (ii) MOLECULE TYPE: peptide
219
220
221       (ix) FEATURE:
222             (A) NAME/KEY: Peptide
223             (B) LOCATION: 1..68
224             (D) OTHER INFORMATION: /note= "AP2-R2 direct repeat at
225                                    positions 221 to 288"
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227       (ix) FEATURE:
228             (A) NAME/KEY: Region
229             (B) LOCATION: 33..50
230             (D) OTHER INFORMATION: /note= "putative AP2-R2 amphipathic
231                                    alpha-helix (SEQ ID NO:7)"
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233
234       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
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236        Ser Ser Lys Tyr Arg Gly Val Thr Leu His Lys Cys Gly Arg Trp Glu
237        1               5               10              15
238
239        Ala Arg Met Gly Gln Phe Leu Gly Lys Lys Tyr Val Tyr Leu Gly Leu
240                 20              25              30
241
242        Phe Asp Thr Glu Val Glu Ala Ala Arg Ala Tyr Asp Lys Ala Ala Ile
243                 35              40              45
244
245        Lys Cys Asn Gly Lys Asp Ala Val Thr Asn Phe Asp Pro Ser Ile Tyr
246             50              55              60
247
248        Asp Glu Glu Leu
249        65
250
251
252   (2) INFORMATION FOR SEQ ID NO:6:
253
254        (i) SEQUENCE CHARACTERISTICS:
255             (A) LENGTH: 18 amino acids
256             (B) TYPE: amino acid
257             (C) STRANDEDNESS:
258             (D) TOPOLOGY: linear
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/879,827A*

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